

WEST Search History

DATE: Wednesday, February 02, 2005

Hide?	Set Name	Query	Hit Count
		<i>DB=PGPB,USPT,USOC,EPAB,JPAB,DWPI; PLUR=YES; OP=ADJ</i>	
<input type="checkbox"/>	L1	tamura-T\$.in.	8783
<input type="checkbox"/>	L2	oto-N\$.in. or suzuki-N\$.in. or mizuno-K\$.in. L1	12951
<input type="checkbox"/>	L3	oto-N\$.in. or suzuki-N\$.in. or mizuno-K\$.in.	17323
<input type="checkbox"/>	L4	yamamoto-N\$.in. or suzuki-N\$.in. or mizuno-K\$.in.	24242
<input type="checkbox"/>	L5	(L1 or L4) and (biochip or array)	682
<input type="checkbox"/>	L6	(L1 or L4) and (biochip or microarray or array)	697
<input type="checkbox"/>	L7	L6 and hybridiz\$	62
<input type="checkbox"/>	L8	L7 and biopolymer	20
<input type="checkbox"/>	L9	L8 and visual\$	7
<input type="checkbox"/>	L10	probe similarity score	0
<input type="checkbox"/>	L11	similarity score	1108
<input type="checkbox"/>	L12	biochip or microarray	16282
<input type="checkbox"/>	L13	L12 same bipolymer	1
<input type="checkbox"/>	L14	L11 and L12	62
<input type="checkbox"/>	L15	L14 and biopolymer	13
<input type="checkbox"/>	L16	L15 and (imag\$ and visual\$)	9
<input type="checkbox"/>	L17	L16 and hybridiz\$	9
<input type="checkbox"/>	L18	L12 and biopolymer	1568
<input type="checkbox"/>	L19	L18 and hybridiz\$	1399
<input type="checkbox"/>	L20	L19 and (similar\$ scor\$ or percent homology or percent identity or sequence identity)	491
<input type="checkbox"/>	L21	L20 and (display\$ and imag\$ and visual\$)	295
<input type="checkbox"/>	L22	L21 and (different same color)	26
<input type="checkbox"/>	L23	L22 and (different same (valu\$ or depth))	20
<input type="checkbox"/>	L24	L23 and spot imag\$	1
<input type="checkbox"/>	L25	L23 and statistic\$	20
<input type="checkbox"/>	L26	L25 and matrix	18
<input type="checkbox"/>	L27	L26 and (hybridization level or hybridization profile)	1
<input type="checkbox"/>	L28	L25 and storage unit	1
<input type="checkbox"/>	L29	L25 and (data near storage)	7

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS,
BIOTECHNO' ENTERED AT 16:01:12 ON 02 FEB 2005

L1 18530 S (IDENTITY OR SIMILAR? OR HOMOLOG?) (10A) (PROBE OR OLIGOMER O
L2 261 S L1 AND (BLAST OR SIMOTH-WATERSON OR ALGORITHM)
L3 5 S L2 AND (VISUAL? OR GRAPH?)
L4 104 S L2 AND (HYBRIDIZ?)
L5 11 S L4 AND (DISPLAY OR VISUAL? OR GRAPH? OR REPRESENTATION OR CO

=> s biochip same (probe or oliomer or biopolymer or oligonucleotide)

MISSING OPERATOR 'SAME (PROBE'

The search profile that was entered contains terms or
nested terms that are not separated by a logical operator.

=> s biochip (6a) (probe# or oliomer# or biopolymer# or oligonucleotide#)

L6 426 BIOCHIP (6A) (PROBE# OR OLIOMER# OR BIOPOLYMER# OR OLIGONUCLEOTI
DE#)

=> s l6 an(Blast or Smith-Watsonson or algorithm)

<-----User Break----->

(FILE 'HOME' ENTERED AT 16:00:23 ON 02 FEB 2005)

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS, BIOTECHNO' ENTERED AT 16:01:12 ON 02 FEB 2005

L1 18530 S (IDENTITY OR SIMILAR? OR HOMOLOG?) (10A) (PROBE OR OLIGOMER O
L2 261 S L1 AND (BLAST OR SIMOTH-WATERSON OR ALGORITHM)
L3 5 S L2 AND (VISUAL? OR GRAPH?)
L4 104 S L2 AND (HYBRIDIZ?)
L5 11 S L4 AND (DISPLAY OR VISUAL? OR GRAPH? OR REPRESENTATION OR CO
L6 426 S BIOCHIP (6A) (PROBE# OR OLIOMER# OR BIOPOLYMER# OR OLIGONUCLE

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS, BIOTECHNO' ENTERED AT 16:27:42 ON 02 FEB 2005

L7 6955782 S (IDENTITY OR SIMILAR? OR HOMOLOG? OR SIMILARITY SCORE)
L8 18530 S L1 (10A) (PROBE OR OLIGOMER OR OLIGONUCLEOTIDE OR BIOPOLYMER)
L9 261 S L8 AND (BLAST OR SMITH-WATERSON OR ALGORITHM)
L10 39 S L9 AND (BIOCHIP OR ARRAY OR CHIP OR MICROARRAY OR HYBRIDIZAT
L11 26 DUP REM L10 (13 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 16:40:03 ON 02 FEB 2005

FILE 'MEDLINE, BIOTECHDS, EMBASE, BIOSIS, SCISEARCH, CANCERLIT, CAPLUS, BIOTECHNO' ENTERED AT 16:45:11 ON 02 FEB 2005

L12 0 S PROBE VERSUS PROBE
L13 2142 S PROBE (5A) COMPARISON
L14 31 S L13 AND ALGORITHM
L15 10 S L14 AND (IDENTITY OR SIMILAR? OR HOMOLOG? OR SIMILARITY SCOR
L16 510538 S (BLAST OR SMITH-WATERSON OR ALGORITHM)
L17 17831 S L16 AND (ARRAY OR MICROARRAY OR BIOCHIP OR CHIP OR HYBRIDIZA
L18 33 S L17 AND (LEVEL (3A) HYBRIDIZ?)
L19 3139 S L17 AND (DISPLAY? OR GRAPH? OR CLUSTER?)
L20 3 S L18 AND (CLUSTER?)

FILE 'STNGUIDE' ENTERED AT 16:55:13 ON 02 FEB 2005

=>

123:331092

TITLE: DNA sequence recognition by hybridization to short oligomers
AUTHOR(S): Milosavljevic, Aleksandar
CORPORATE SOURCE: Center Biol. Biotechnology, Argonne National Lab., Argonne, IL, 60439-4833, USA
SOURCE: Journal of Computational Biology (1995), 2(2), 355-70
CODEN: JCOBEM; ISSN: 1066-5277
PUBLISHER: Liebert
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A format 1 technol. for performing massive hybridization expts. has been developed as part of the sequencing by hybridization (SBH) project. Arrays of tens of thousands of clones are interrogated with short oligomer probes to determine sets of oligomers that are present in individual clones. SBH requires highly discriminative hybridizations with a large number of probes. One of the main uses of a reconstructed DNA sequence is in a similarity search against databases of known DNA. The authors argue that sequence reconstruction, even partial, should not be performed for this particular purpose; the authors provide an information-theoretic proof that the **oligomer** lists obtained from hybridization expts. should be used directly for **similarity** searches. The authors propose a similarity search method that takes full advantage of the subword structure of pos. identified oligomers within a clone. The method tolerates error in hybridization expts., requires fewer probes than necessary for sequencing, and is computationally efficient. To enable direct sequence recognition, the authors apply the recently developed method of sequence comparison that is based on minimal length encoding and algorithmic mutual information. The method has been tested on both real and simulated data and has led to a correct identification of clones based on hybridizations with 109 short oligomer probes. The method is applicable to hybridization data that comes from both format 1 and format 2 (sequencing **chip**) hybridization expts. The sequence recognition method can provide targeting information for large-scale DNA sequencing by gel-based methods or by hybridization.

Computers & Chemistry

Volume 23, Issues 3-4 , 15 June 1999, Pages 251-262

This Document

► **Abstract**

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An **algorithm** for the assembly of robust physical maps based on a combination of multi-level **hybridization** data and fingerprinting data.

AUTHOR: Sasinowska H; Sasinowski M

CORPORATE SOURCE: Department of Mathematical Sciences, Clemson University, Clemson, SC 29634, USA.. heather@math.clemson.edu

SOURCE: Computers & chemistry, (1999 Jun 15) 23 (3-4) 251-62.
Journal code: 7607706. ISSN: 0097-8485.

PUB. COUNTRY: ENGLAND: United Kingdom

DOCUMENT TYPE: Journal; Article; (JOURNAL ARTICLE)

LANGUAGE: English

FILE SEGMENT: Priority Journals

ENTRY MONTH: 200001

ENTRY DATE: Entered STN: 20000114
Last Updated on STN: 20000114
Entered Medline: 20000104

AB We have developed an **algorithm** which combines data obtained from restriction digestion experiments and **hybridization** experiments to construct robust physical maps of whole chromosomes. The **algorithm** has been incorporated into a program which accepts **hybridization** data consisting of an unordered **hybridization** matrix and fingerprinting data containing band coordinates for each clone. The combined data is used to produce a non-redundant, ordered matrix which can be further reduced to represent a minimum tile coverage of the chromosome. In addition, the method also takes into account multi-level **hybridization** events which allows for an improved treatment of the **hybridization** data. The program is evaluated against several other contig building programs using simulated and real data sets. Finally, it is applied to construct a physical map of the 4.1 Mb genome of *Ochrobactrum anthropi* based on 1387 clones and 70 probes, as well as 624 fingerprints.

=> FIL STNGUIDE

COST IN U.S. DOLLARS	SINCE FILE	TOTAL
	ENTRY	SESSION
FULL ESTIMATED COST	99.10	331.93
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AND TECHNOLOGY CORPORATION, AND FACHINFORMATIONSZENTRUM KARLSRUHE

FILE CONTAINS CURRENT INFORMATION.
LAST RELOADED: Jan 28, 2005 (20050128/UP).

=>

<input type="checkbox"/>	L30	L25 and hybridization	20
<input type="checkbox"/>	L31	((biopolymer or probe) near (biochip or microarray))	188
<input type="checkbox"/>	L32	L31 and ((display\$ or visual\$) same hybridiz\$)	14
<input type="checkbox"/>	L33	(display\$ or visual\$) same (percent identity or percent homology or sequence identity or sequence similarity or similarity score)	3047
<input type="checkbox"/>	L34	L33 same (hybridization)	105
<input type="checkbox"/>	L35	L34 and (graphic\$)	11
<input type="checkbox"/>	L36	L33 and (different near color)	57
<input type="checkbox"/>	L37	L36 and (image)	36
<input type="checkbox"/>	L38	L31 and L33	23
<input type="checkbox"/>	L39	(display\$ or visual\$)near(percent identity or percent homology or sequence identity or sequence similarity or similarity score)	130
<input type="checkbox"/>	L40	L39 and hybridiz\$	101
<input type="checkbox"/>	L41	L40 and (biochip or microarray)	21
<input type="checkbox"/>	L42	L41 and (biopolymer or probe)	21
<input type="checkbox"/>	L43	L39 and (biochip or microarray)	21
<input type="checkbox"/>	L44	L33 and (biochip or microarray)	467
<input type="checkbox"/>	L45	L44 and hybridization	436
<input type="checkbox"/>	L46	L45 and ((Imag\$ or matrix or graphic\$) same (different near color))	1
<input type="checkbox"/>	L47	L45 and ((Imag\$ or matrix or graphic\$) and (different near color))	6
<input type="checkbox"/>	L48	BLAST-same (imag\$ or graphic\$ or visual\$)	4304
<input type="checkbox"/>	L49	L48 same (biochip or micrarray)	5
<input type="checkbox"/>	L50	6188783.pn. or 5812272.pn. or 6471916.pn. or 6284465.pn.	8
<input type="checkbox"/>	L51	6349144.pn. or 4852183.pn. or 6306643.pn. or 6228575.pn.	8
<input type="checkbox"/>	L52	(identity or similarity) near score	2210
<input type="checkbox"/>	L53	L52 same probe\$	12
<input type="checkbox"/>	L54	L52 and l48	22
<input type="checkbox"/>	L55	L54 and prob\$	21
<input type="checkbox"/>	L56	L52 and (BLAST or smith-watson or algorithm)	1790
<input type="checkbox"/>	L57	L52 same (probe or oligonucleotide or biopolymer or oligomer)	18

END OF SEARCH HISTORY